REMARKS

Applicants hereby submit that the enclosures fulfill the requirements under 37 C.F.R. §1.821-1.825. The amendments in the specification merely insert the paper copy of the Sequence Listing and sequence identifiers in the specification. No new matter has been added.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing attorney docket no. 13687-002001.

Respectfully submitted,

Date: 1-29-02

Y. Rocky Tsao
Y. Rocky Tsao
Reg. No. 34,053

Fish & Richardson P.C.
225 Franklin Street
Boston, Massachusetts 02110-2804
Telephone: (617) 542-5070
Facsimile: (617) 542-8906

20380840.doc

"Version With Markings to Show Changes Made"

In the specification:

Paragraph beginning at page 10, line 3, has been amended as follows:

Fig. 6 shows the DNA sequence of the *Agrobacterium rhizogenes rolC* gene (SEQ ID NO:1).

Paragraph beginning at page 10, line 29, has been amended as follows:

Fig. 12 shows the cDNA sequece of *fht* from carnation (SEQ ID NO:2).

Paragraph beginning at page 10, line 30, has been amended as follows:

Fig. 13 shows the sequence of the antisense fragment to the *fht* cDNA (SEQ ID NO:3).

Paragraph beginning at page 16, line 17, has been amended as follows:

DNA extraction, primers for *uidA*, and PCR conditions were as previously described (Tzfira T, Jensen CS, Wangxia W, Zuker A, Altman A, Vainstein A: Transgenic Populus: a step-by-step protocol for its *Agrobacterium*-mediated transformation. (1997) Plant Mol Biol Rep 15:219-235). The primers for *nptII* amplification were 5'-GAGGCTATTCGGCTATGACT-3' (SEQ ID NO:4) and 5'-AATCTCGTGATGGCAGGTTG-3' (SEQ ID NO:5). The predicted sizes of the amplified DNA fragments were 0.53 kb and 0.8 kb for *uidA* and *nptII*, respectively. Amplified DNA was electrophoresed on a 1.5% (w/v) agarose gel, using Tris-borate buffer (1.3 M Tris, 0.7 M boric acid and 24.5 mM EDTA, pH 8.4). Gels were stained with ethidium bromide, photographed under ultraviolet light, and analyzed by Southern blotting.

Paragraph beginning at page 30, line 22, has been amended as follows:

Carnation cDNA clones of *chs* and *dfr* were isolated, as described above for FHT, by PCR using specific primers according to their sequences in GenBank: *chs* (Z67982), *dfr* (Z67983). Primers used were: 5' CCC AAA ACG CTC ACT TCA CT 3' (SEQ ID NO:6) and 5' CCA AGC CCA TCT AAG CAA GT 3' (SEQ ID NO:7) for *fht*; 5' GGG CCG ATG GTC

CTG CTA CTA T 3' (SEQ ID NO:8) and 5' ACG CGC TCG ACA TGT TCC CAA A 3' (SEQ ID NO:9) for *chs*; 5' TGT GAA TGT CGA AGC GAC TC 3' (SEQ ID NO:10) and 5' TTG AAT TTG GTG GGG ACA TT 3' (SEQ ID NO:11) for *dfr*.